with sister when possible, less often brother with half-sister, rarely cousin with cousin. In this way were obtained 804 young from rigidly selected, closely inbred descendants of a single pair of rats, the series extending into generation F_8. We have shown (*l. c.*, p. 21) that the progress of selection within this inbred family follows a remarkably close parallel, generation by generation, to the progress of selection in our plus series as a whole. Muller's anticipation that a different result would follow close inbreeding is not justified by our observations.

In discussing this experiment (p. 21) we have italicized the statement that (so far as the hooded character is concerned) *the entire series is derived from a single hooded individual!* When the Hagedoorns made the statement that our stock had not been sufficiently inbred, they had apparently not seen our full publication and so had no means of knowing to what extent it had been inbred, but Muller, with our full publication before him, apparently repeats the statement without taking the trouble to verify it.

W. E. CASTLE

BUSSEY INSTITUTION,
October 23, 1914

NO CROSSING OVER IN THE FEMALE OF THE SILKWORM MOTH

IN a recent review[1] of a paper by Y. Tanaka[2] on linkage in the silkworm moth, I pointed out that some of his data suggested that crossing over was occurring in only one sex. While the data were not sufficient to establish this conclusion, there was at this time another paper by the same author[3] which I had not seen. In this paper are presented data which clear up the matter.

Tanaka has now made back-cross tests of both sexes. That crossing over does occur in the males was shown by the mating sysy ♀ × SYsy ♂, which gave a total of 865 cross-overs among 2,907 offspring. The cross sysy ♀ × SysY ♂ gave 151/488 as the proportion of cross-overs. But when females were tested, SYsy ♀ × sysy ♂ gave no cross-overs in 1,183 offspring. Tanaka refers to another paper, apparently in press, in which he has shown the same relations (*i. e.*, crossing over in males, none in

[1] AMER. NAT., XLVIII, 1914.

[2] *Jour. Coll. Agr. Tohoku Imp. Univ. Sapporo,* V, 1913.

[3] *Jour. Coll. Agr. Tohoku Imp. Univ. Sapporo,* VI, 1914.

females) for the combinations NynY and MYmy. As stated in my former review, there was in the earlier paper a record of the mating sysy ♀ × SysY ♂, giving no cross-overs in 128 offspring. Tanaka now says, referring to this case: "Whether there may exist, in certain occasion, a complete reduplication [linkage] in *male,* or whether the above result is due to any mistake by which sex-signs have been reversed, is at present uncertain. No similar case has as yet been found in other families."

The evidence seems to make it highly probable that crossing over in the silkworm moth occurs only in the male; a surprising result when we remember that in *Drosophila* it occurs only in the *female.* One is immediately reminded that in *Drosophila* the male is heterozygous for the sex-differentiator, while in *Abraxas* and probably all moths the female is the heterozygous sex. These facts are highly suggestive, and lead one to wonder what will be found with regard to crossing over in the two sexes in birds and mammals, where similar differences in sex-determination occur. Another point worth noting in this connection is that in the hermaphroditic sweet pea and *Primula* crossing over occurs in the formation both of pollen and of ovules.

Tanaka reports two cases of aberrant results which, as he says, may be explained as due to mutation ("dropping out") of S in one case, and of both S and Y in the other. He adds that such an assumption is premature. To the writer it seems more probable that the females involved were not virgin. The results are easily explained on the assumption that they had paired with brothers before isolation, since brothers of the necessary composition are shown by the pedigrees to have been present in each case.

Another interesting point brought out by Tanaka's more recent paper is the relation between the larval patterns known as striped, moricaud, normal, and plain. In my earlier review I followed Tanaka in treating these patterns as affected by three pairs of genes: S (striped) and s, M (moricaud) and m, and N (normal) and n, plain being the triple recessive. The same scheme has been followed in the early part of this paper. On this assumption, as Tanaka points out, it is necessary to suppose that complete linkage occurs between these three pairs of genes. The evidence need not be gone over in detail here, but there are over 10,000 larvæ recorded from various tests of this relation, without a single cross-over among them. Although Tanaka does not mention the point, this at once brings up the possibility that

we may be dealing with a system of multiple allelomorphs. No two of the types when mated together give a third in F_1; and, unless one or both carry a recessive in heterozygous form, any two types give a 3:1 ratio in F_2, or 1:1 on back-crossing to a recessive. The four patterns involved seem, from the descriptions, to fall roughly into a series in the order striped, moricaud, normal, and plain. That is to say, the second two are rather intermediate in appearance between striped and plain. Although I believe any arguments as to the nature of genes which are based on the appearance of characters are open to very serious objections, it must still be admitted that the different characters involved in a case of multiple allelomorphism are generally of the same sort.[4]

On the chromosome view, if the genes just discussed are allelomorphs they occupy identical loci in homologous chromosomes. If they are not allelomorphic but closely linked, they occupy different but closely opposed loci in homologous chromosomes. In either case, any combination of them should give approximately the same linkage to the Y–y pair of genes, which occupy a locus in the same chromosome, but some distance away. The linkage of the striped-normal, striped-plain, and moricaud-plain combinations with the Y–y locus appear from Tanaka's data to be in fact about the same, though the data on the first (striped-normal) are the only ones sufficiently large to be very significant.

A. H. STURTEVANT

COLUMBIA UNIVERSITY,
October, 1914

THE INFLUENCE OF POSITION IN THE POD UPON THE WEIGHT OF THE BEAN SEED

IN a note on the pure line problem Belling[1] has emphasized the significance of position in the pod as a factor in determining the weight of the bean seed. Since this point in his paper seems to have attracted some attention among those interested in genetics, it may not be out of place to call attention to a series of quantitative determinations of the intensity of the relationship[2] and to illustrate the results secured.

If one numbers the successive ovules of the pod from 1 up,

[4] I have discussed this aspect of the matter briefly in another paper (AMER. NAT., XLVII, 1913, p. 237).

[1] Belling, J., "Selection in Pure Lines," *Amer. Breed. Mag.*, 3: 311–312, 1912.

[2] Harris, J. Arthur, "A Quantitative Study of the Factors Influencing the